

SEQUENCE LISTING

<110> Daniel E. Afar
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<120> NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
AND THERAPY OF PROSTATE AND COLON CANCER

<130> 129.8USU1

<140> 09/323,597

<141> 1999-06-01

<150> 60/087,598

<151> 1998-06-01

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<151> 1998-06-29

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<151> 1999-04-14

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                                     Met Ala
                                     1

ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat      165
Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
      5              10              15

gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc      213
Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
      20              25              30

act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc      261
Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
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cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc
Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys
55 60 65

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Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys
70 75 80

aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct
Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala
85 90 95

gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc
Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser
100 105 110

aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct
Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser
115 120 125 130

aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat
Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn
135 140 145

cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca
Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser
150 155 160

tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag
Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu
165 170 175

aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt
Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe
180 185 190

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Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met
195 200 205 210

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Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr
215 220 225

cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata
His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile
230 235 240

gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc
Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly
245 250 255

ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac
Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His
260 265 270

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693

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837

885

933

C1
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atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg 1029
Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp
295 300 305

cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat 1077
His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr
310 315 320

gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac 1125
Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp
325 330 335

tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct 1173
Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro
340 345 350

ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc 1221
Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly
355 360 365 370

atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg gcc 1269
Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala
375 380 385

acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg 1317
Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val
390 395 400

ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac aac 1365
Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn
405 410 415

ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc 1413
Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val
420 425 430

gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac 1461
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn
435 440 445 450

aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc 1509
Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala
455 460 465

aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg gac 1557
Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp
470 475 480

tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc 1608
Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
485 490

ttgacgtcgt tttacaagaa aacaatgggg ctggttttgc ttccccgtgc atgatttact 1668

C1
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 <213> Homo sapiens

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 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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<220>
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 <222> (57)...(1533)

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 Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
 5 10 15

cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc 155
 His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
 20 25 30

ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg 203
 Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
 35 40 45

ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc 251
 Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
 50 55 60 65

tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act 299
 Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
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 Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
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 Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys
 100 105 110

tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc 443
 Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro
 115 120 125

tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag 491
 Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu
 130 135 140 145

aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac 539
 Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met Tyr
 150 155 160

tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac 587
 Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn
 165 170 175

gag aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat 635
 Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn
 180 185 190

ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt 683
 Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe
 195 200 205

atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg 731
 Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu
 210 215 220 225

tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt 779
 Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys
 230 235 240

tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg 827
 Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val
 245 250 255

ggc ggt gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg 875
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 260 265 270

cac gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag 923
 His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu
 275 280 285

tgg atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca 971
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 290 295 300 305

tgg cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc 1019
 Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe
 310 315 320

tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat 1067
 Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn Tyr
 325 330 335

gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag 1115

Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys
 340 345 350

cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca 1163
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 Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly
 370 375 380 385

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 Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys
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 405 410 415

aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac 1355
 Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn
 420 425 430

gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tgc aac 1403
 Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Asn
 435 440 445

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 Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys
 450 455 460 465

gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg 1499
 Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr
 470 475 480

gac tgg att tat cga caa atg aag gca aac ggc t aatccacatg 1543
 Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
 485 490

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 <212> PRT
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		20					25					30			
Val	Pro	Thr	Val	Tyr	Glu	Val	His	Pro	Ala	Gln	Tyr	Tyr	Pro	Ser	Pro
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Val	Pro	Gln	Tyr	Ala	Pro	Arg	Val	Leu	Thr	Gln	Ala	Ser	Asn	Pro	Val
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Thr	Lys	Lys	Ala	Leu	Cys	Ile	Thr	Leu	Thr	Leu	Gly	Thr	Phe	Leu	Val
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Gly	Ala	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys
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Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn
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Pro	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp
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Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met
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Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp
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		180					185					190			
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	210					215					220				
Leu	Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg
225					230				235					240	
Cys	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile
			245					250					255		
Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser
		260						265					270		
Leu	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro
		275				280						285			
Glu	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn
	290					295					300				
Pro	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met
305					310					315				320	
Phe	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn
			325					330					335		
Tyr	Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln
			340					345				350			
Lys	Pro	Leu	Thr	Phe	Asn	Asp	Leu	Val	Lys	Pro	Val	Cys	Leu	Pro	Asn
		355					360					365			
Pro	Gly	Met	Met	Leu	Gln	Pro	Glu	Gln	Leu	Cys	Trp	Ile	Ser	Gly	Trp
	370				375						380				
Gly	Ala	Thr	Glu	Glu	Lys	Gly	Lys	Thr	Ser	Glu	Val	Leu	Asn	Ala	Ala
385					390					395				400	
Lys	Val	Leu	Leu	Ile	Glu	Thr	Gln	Arg	Cys	Asn	Ser	Arg	Tyr	Val	Tyr
			405					410					415		

cl
Cont

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
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 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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 gcacctgcag cggctgccct ctggggccac ttggtagtgt cccagccta cctctccaca 180
 aggggatttt gctgatgggt tcttanagcc ttagcagccc tggatgggtg ccagaaataa 240
 agggaccagc ccttcatggg tggtagcgtg gtantcactt gtaaggggaa cagaaacatt 300
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 ggaacttgcc ctgagcactc ctggtgca 388

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<213> Artificial Sequence

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<223> Nested Primer (NP) 2

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<210> 12
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<210> 13
<211> 25
<212> DNA
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<220>
<223> RT-PCR Primer 1B

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25